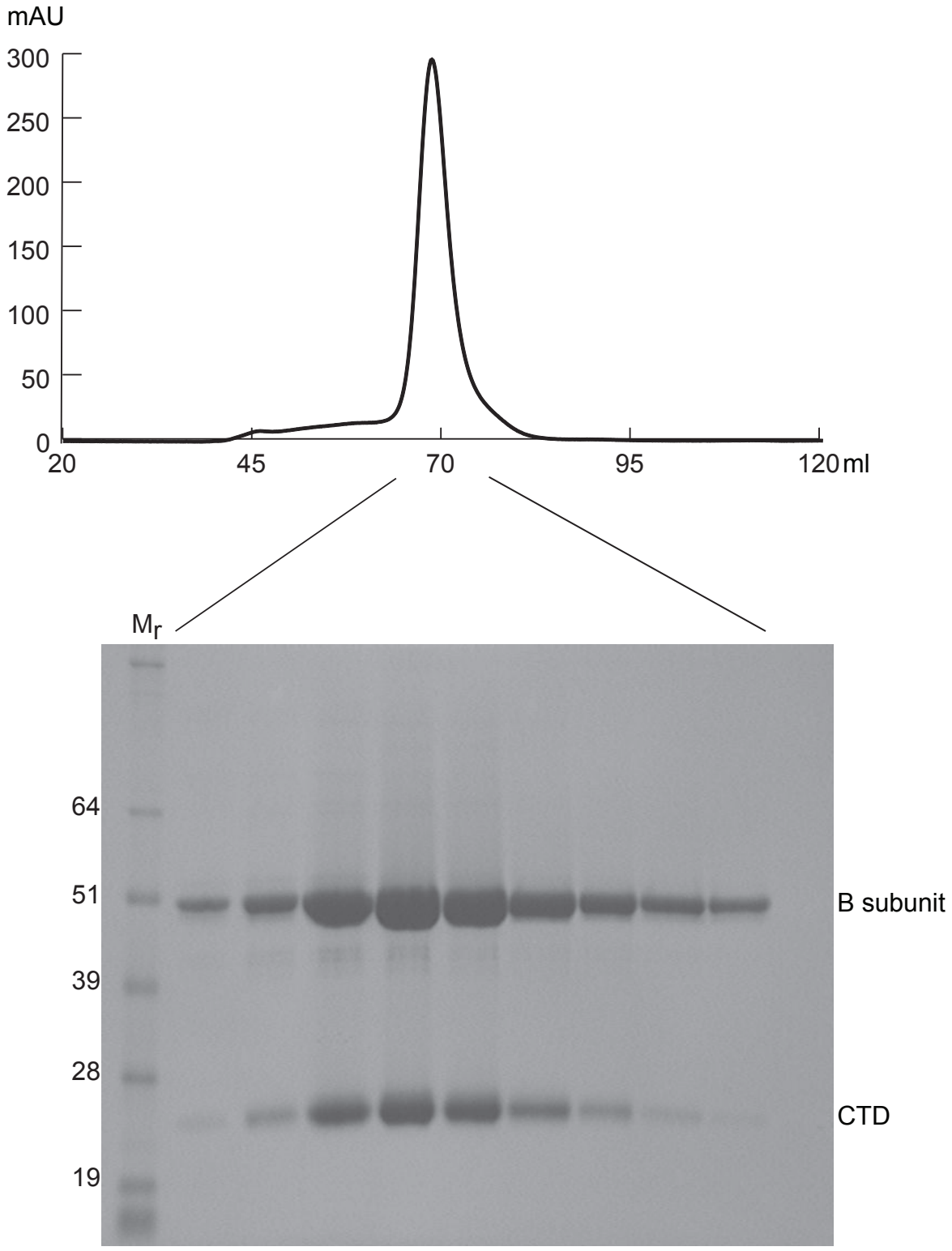
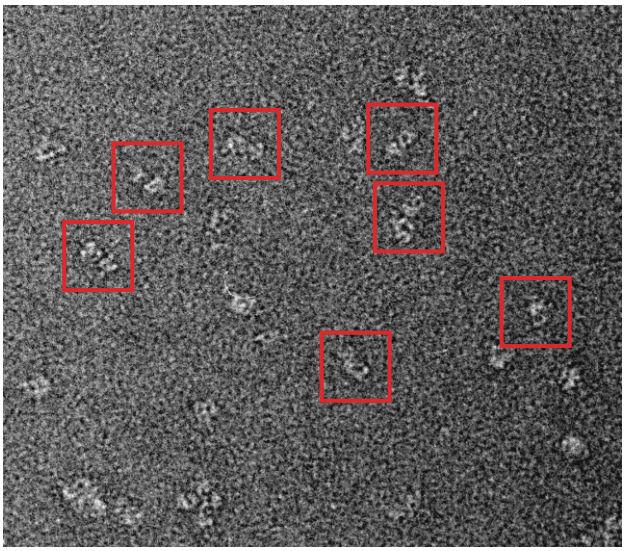


Supplementary figure 1

A



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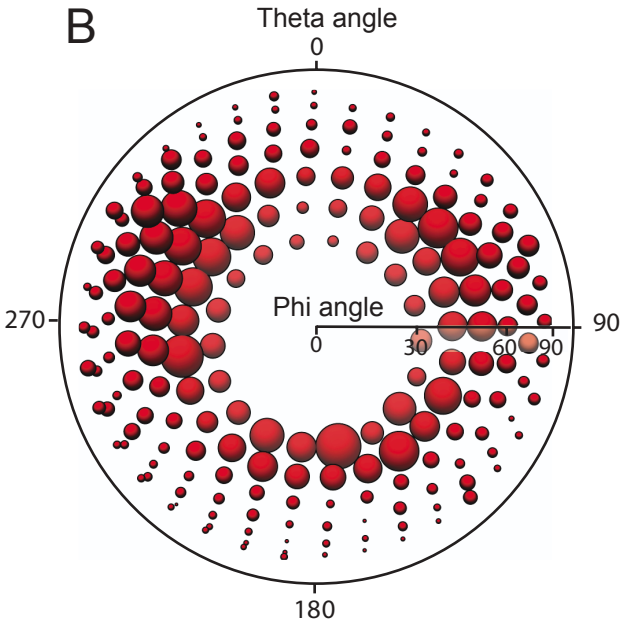
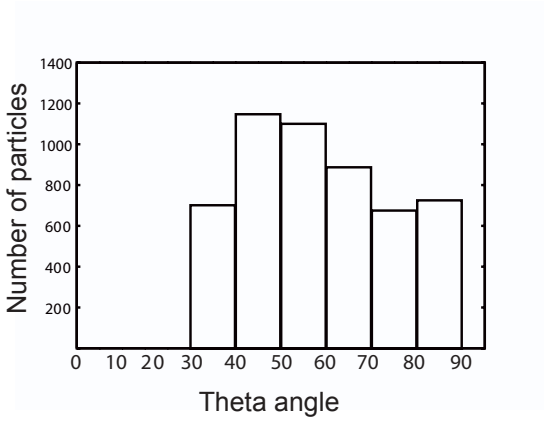
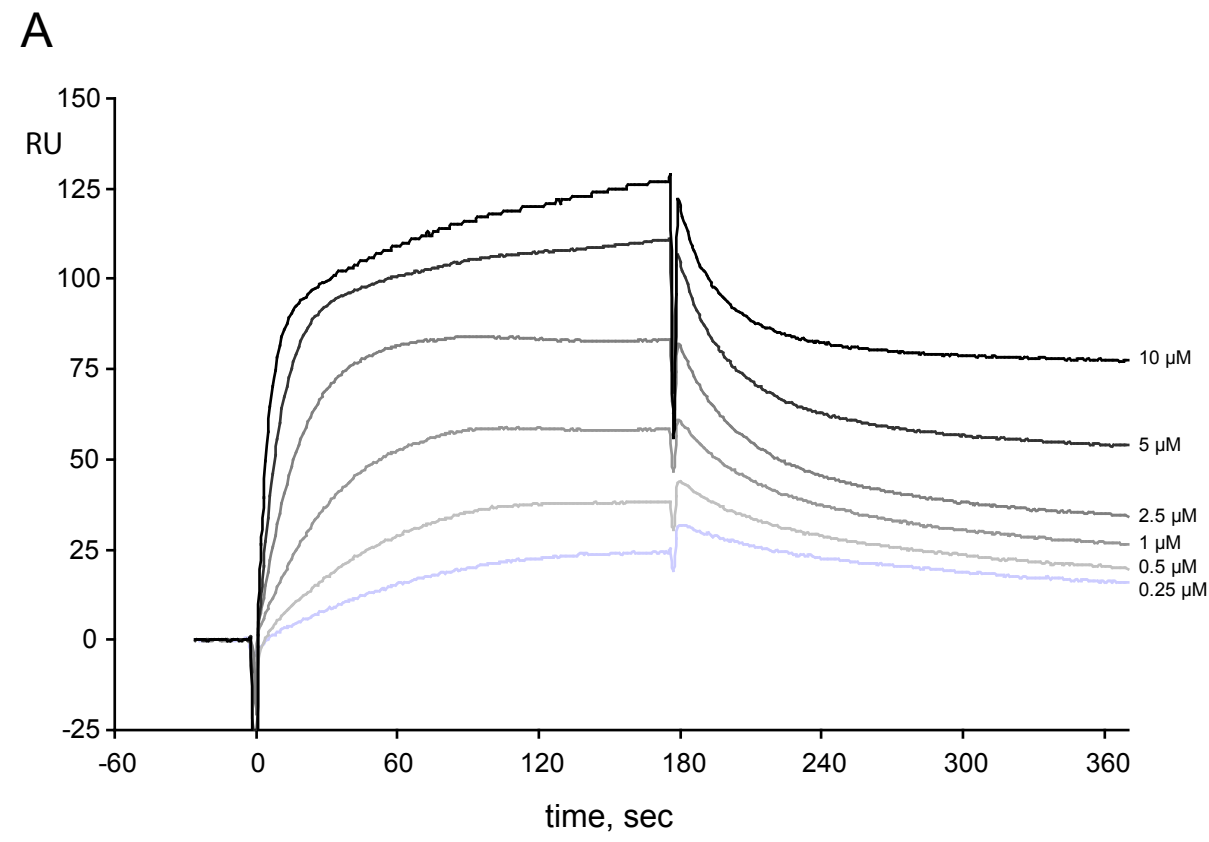
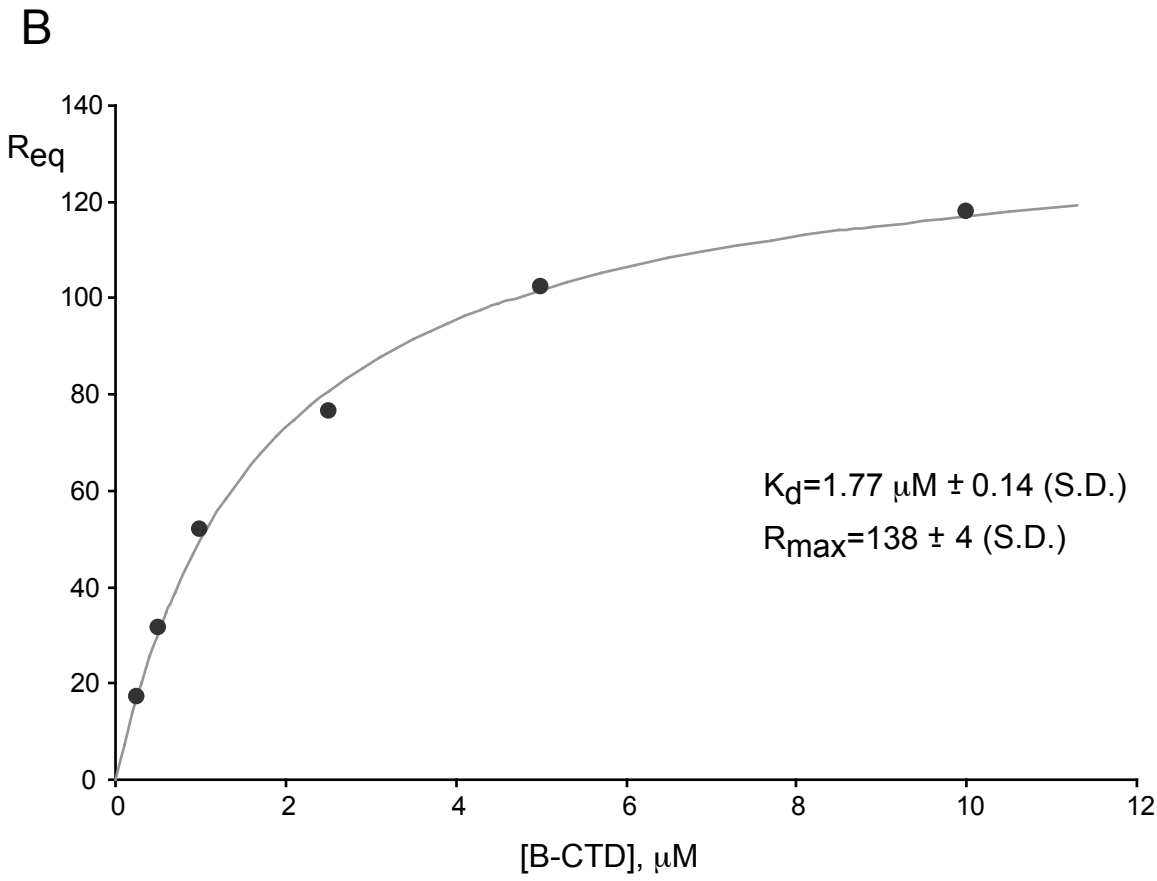




Supplementary figure 2





Supplementary figure 3

Supplementary Figure Legend

Figure 1 Biochemical reconstitution of the CTD - B complex for crystallographic analysis. (**A**) Gel filtration profile of the CTD - B complex on Superdex 200 16/60 column (GE Healthcare). (**B**) SDS-PAGE analysis of fractions corresponding to gel filtration peak.

Figure 2 Image processing of the heterodimeric yeast Pol α. (**A**) A representative field from an electron micrograph obtained for Pol α. Some representative particles are highlighted within a box. (**B**) Angular coverage of the particles used in the reconstruction. As in the case of other complexes that rotate along their longitudinal axis, such as GroEL, a 3D reconstruction can be built from side views corresponding to rotations along that axis. Image processing was performed with side views only, which were found to cover all possible rotations along the longitudinal axis combined with some tilting of the specimen. In the representation at the left, the radius of each sphere represents the number of particles assigned to each orientation. The centre of the circle is empty since top views of the complex were not selected. The panel at the right shows the number of particles for every 10º of the tilt angle.

Figure 3 Surface Plasmon Resonance analysis of the CTD - B interaction with double-stranded DNA. (**A**) SPR runs at several concentrations of the CTD - B complex. Only the first 3 minutes of the dissociation phase is shown. (**B**) The RU values at equilibrium (R_{eq}) plotted against CTD - B complex concentration. The curve is a fit to the data using the model described by Lin et al. (2005). The errors for K_d and R_{max} are 1 standard deviation.

Supplementary Methods

Surface Plasmon Resonance (SPR)

Interaction of the CTD - B complex with dsDNA was performed on a BIAcore 2000 SPR biosensor (BIAcore; GE Healthcare). A biotinylated 26bp-long dsDNA was generated by annealing a pair of complementary oligos (Sigma Genosys), one of which was labelled with biotin at the 5'-end (5'-Biotin-CGTGACTACTGTAAGTCGATGATCCG-3'). The biotinylated dsDNA in TE buffer (10 mM Tris-HCl pH 8.0, 1 mM EDTA) was attached to a streptavidin-coated sensor-chip (Biacore, GE Healthcare) at a flow rate of 20 µl/min, to a level of 400 resonance units (RU). SPR runs with the CTD-B complex were performed in buffer: 20 mM Tris·HCl pH 8.0, 10 mM $MgCl_2$, 50 mM NaCl, 0.1 mM EDTA, 1 mM DTT and 0.05% P20 (Biacore, GE Healthcare) at 30 µl/min. The CTD - B complex was injected over the chip surface for 180 seconds and allowed to dissociate for 15 minutes. The sensor-chip surface was regenerated between runs with a 60s injection of 0.05% SDS. The data was analysed using a steady-state affinity model as described (Lin et al, 2005).

Lin LP, Huang LS, Lin CW, Lee CK, Chen JL, Hsu SM, Lin S (2005) Determination of binding constant of DNA-binding drug to target DNA by surface plasmon resonance biosensor technology. *Curr Drug Targets Immune Endocr Metabol Disord* **5**: 61-72

Supplementary Table 1 Crystallographic data and statistics[a]

Diffraction data			
Data set		Seleno-Methionine	Native
Space Group		$P2_1$	$P2_1$
Unit Cell Parameters (Å)	a	85.0	85.9
	b	142.9	143.0
	c	175.5	175.6
	β	102.1°	102.2°
Resolution (Å)		2.8	2.5
		Peak	
Wavelength (Å)		0.98020	1.2852
Unique reflections		100963	141597
Completeness (%)		100.0 (100.0)	98.8 (98.7)
Multiplicity		7.2 (7.3)	7.3 (7.4)
R_{meas} (%)[b]		14.8 (61.2)	11.0 (70.0)
R_{pim} (%)[c]		7.5 (31.8)	4.0 (26.0)
I/σ(I))		4.7 (1.3)	5.2 (1.2)

Refinement statistics	
Resolution (Å)	2.5
Number of unique reflections	134185
Number of non-H atoms	20650
R_{factor} (%)[d]	19.2 (31.3)
R_{free} (%)[e]	21.8 (36.5)
Average B-factor, all atoms (Å^2)	52.7
Number of waters	571
R.m.s. deviation bond lengths (Å)	0.016
R.m.s. deviation bond angles (°)	1.545

[a] Number in parentheses refer to the outermost shell.

[b]
$$R_{meas} = \frac{\sum_{hkl} \sqrt{\frac{n}{n-1}} \sum_i \left| I_{i,hkl} - \langle I_{i,hkl} \rangle \right|}{\sum_{hkl} \sum_i I_{i,hkl}}$$

[c]
$$R_{pim} = \frac{\sum_{hkl} \sqrt{\frac{1}{n-1}} \sum_i \left| I_{i,hkl} - \langle I_{i,hkl} \rangle \right|}{\sum_{hkl} \sum_i I_{i,hkl}}$$

[d]
$$R\text{-factor} = \frac{\sum_{hkl} \left| |F_{obs}| - |F_{calc}| \right|}{\sum_{hkl} |F_{obs}|}$$

[e] Test-set size is 5% of working set (7082 reflections).